> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                                      SEQUENCE LISTING
 2
 3    (1)      General Information:
 4
 5         (i) APPLICANT: Meissner, Paul S.
 6                        Coleman, Timothy A.
 7
 8        (ii) TITLE OF INVENTION: Human Criptin Growth Factor
 9
10       (iii) NUMBER OF SEQUENCES: 7
11
12        (iv) CORRESPONDENCE ADDRESS:
13             (A) ADDRESSEE: Human Genome Sciences, Inc.
14             (B) STREET: 9410 Key West Avenue
15             (C) CITY: Rockville
16             (D) STATE: MD
17             (E) COUNTRY: USA
18             (F) ZIP: 20850
19
20         (v) COMPUTER READABLE FORM:
21             (A) MEDIUM TYPE: Floppy disk
22             (B) COMPUTER: IBM PC compatible
23             (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24             (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26        (vi) CURRENT APPLICATION DATA:
27             (A) APPLICATION NUMBER: US 09/393,023
28             (B) FILING DATE: 09-SEP-1999
29             (C) CLASSIFICATION:
30
31       (vii) PRIOR APPLICATION DATA:
32             (A) APPLICATION NUMBER: US 08/471,371
33             (B) FILING DATE: 06-JUN-1995
34
35      (viii) ATTORNEY/AGENT INFORMATION:
36             (A) NAME: Marks, Michelle S.
37             (B) REGISTRATION NUMBER: 41,971
38             (C) REFERENCE/DOCKET NUMBER: PF200D1
39
40        (ix) TELECOMMUNICATION INFORMATION:
41             (A) TELEPHONE: 301-309-8504
42             (B) TELEFAX: 301-309-8439
43
44
45    (2) INFORMATION FOR SEQ ID NO:1:
46
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INPUT SET: S34300.raw

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47        (i) SEQUENCE CHARACTERISTICS:
48            (A) LENGTH: 672 base pairs
49            (B) TYPE: nucleic acid
50            (C) STRANDEDNESS: single
51            (D) TOPOLOGY: linear
52
53       (ii) MOLECULE TYPE: DNA (genomic)
54
55
56       (ix) FEATURE:
57            (A) NAME/KEY: CDS
58            (B) LOCATION: 1..672
59
60
61       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
62
63   ATG ACC TGG AGG CAC CAT GTC AGG CTT CTG TTT ACG GTC AGT TTG GCA        48
64   Met Thr Trp Arg His His Val Arg Leu Leu Phe Thr Val Ser Leu Ala
65    1               5                  10                  15
66
67   TTA CAG ATC ATC AAT TTG GGA AAC AGC TAT CAA AGA GAG AAA CAT AAC        96
68   Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr Gln Arg Glu Lys His Asn
69                20                  25                  30
70
71   GGC GGT AGA GGG GAA GTC ACC AAG GTT GCC ACT CAG AAG CAC CGA CAG       144
72   Gly Gly Arg Gly Glu Val Thr Lys Val Ala Thr Gln Lys His Arg Gln
73             35                  40                  45
74
75   TCA CCG CTT AAC TGG ACC TCC AGT CAT TTC GGA GAG GTG ACT GGG AGC       192
76   Ser Pro Leu Asn Trp Thr Ser Ser His Phe Gly Glu Val Thr Gly Ser
77          50                  55                  60
78
79   GCC GAG GGC TGG GGG CCG GAG GAG CCG CTC CCC TAC TCC CGG GCT TTC       240
80   Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu Pro Tyr Ser Arg Ala Phe
81    65                  70                  75                  80
82
83   GGA GAG GGT GCG TCC GCG CGG CCG CGC TGC TGC AGG AAC GGC GGT ACC       288
84   Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys Cys Arg Asn Gly Gly Thr
85                85                  90                  95
86
87   TGC GTG CTG GGC AGC TTC TGC GTG TGC CCG GCC CAC TTC ACC GGC CGC       336
88   Cys Val Leu Gly Ser Phe Cys Val Cys Pro Ala His Phe Thr Gly Arg
89             100                 105                 110
90
91   TAC TGC GAG CAT GAC CAG AGG CGC AGT GAA TGC GGC GCC CTG GAG CAC       384
92   Tyr Cys Glu His Asp Gln Arg Arg Ser Glu Cys Gly Ala Leu Glu His
93             115                 120                 125
94
95   GGA GCC TGG ACC CTC CGC GCC TGC CAC CTC TGC AGG TGC ATC TTC GGG       432
96   Gly Ala Trp Thr Leu Arg Ala Cys His Leu Cys Arg Cys Ile Phe Gly
97          130                 135                 140
98
99   GCC CTG CAC TGC CTC CCC CTC CAG ACG CCT GAC CGC TGT GAC CCG AAA       480
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INPUT SET: S34300.raw

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100    Ala Leu His Cys Leu Pro Leu Gln Thr Pro Asp Arg Cys Asp Pro Lys
101    145             150             155             160
102

103    GAC TTC CTG GCC TCC CAC GCT CAC GGG CCG AGC GCC GGG GGC GCG CCC    528
104    Asp Phe Leu Ala Ser His Ala His Gly Pro Ser Ala Gly Gly Ala Pro
105                    165             170             175
106

107    AGC CTG CTA CTC TTG CTG CCC TGC GCA CTC CTG CAC CGC CTC CTG CGC    576
108    Ser Leu Leu Leu Leu Leu Pro Cys Ala Leu Leu His Arg Leu Leu Arg
109                    180             185             190
110

111    CCG GAT GCG CCC GCG CAC CCT CGG TCC CTG GTC CCT TCC GTC CTC CAG    624
112    Pro Asp Ala Pro Ala His Pro Arg Ser Leu Val Pro Ser Val Leu Gln
113                    195             200             205
114

115    CGG GAG CGG CGC CCC TGC GGA AGG CCG GGA CTT GGG CAT CGC CTT TAA    672
116    Arg Glu Arg Arg Pro Cys Gly Arg Pro Gly Leu Gly His Arg Leu   *
117                    210             215             220
118

119

120    (2) INFORMATION FOR SEQ ID NO:2:
121

122            (i) SEQUENCE CHARACTERISTICS:
123                    (A) LENGTH: 223 amino acids
124                    (B) TYPE: amino acid
125                    (D) TOPOLOGY: linear
126

127            (ii) MOLECULE TYPE: protein
128

129            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
130

131    Met Thr Trp Arg His His Val Arg Leu Leu Phe Thr Val Ser Leu Ala
132    1               5               10              15
133

134    Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr Gln Arg Glu Lys His Asn
135                    20              25              30
136

137    Gly Gly Arg Gly Glu Val Thr Lys Val Ala Thr Gln Lys His Arg Gln
138            35              40              45
139

140    Ser Pro Leu Asn Trp Thr Ser Ser His Phe Gly Glu Val Thr Gly Ser
141        50              55              60
142

143    Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu Pro Tyr Ser Arg Ala Phe
144    65              70              75              80
145

146    Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys Cys Arg Asn Gly Gly Thr
147                    85              90              95
148

149    Cys Val Leu Gly Ser Phe Cys Val Cys Pro Ala His Phe Thr Gly Arg
150                    100             105             110
151

152    Tyr Cys Glu His Asp Gln Arg Arg Ser Glu Cys Gly Ala Leu Glu His
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/393,023A*

INPUT SET: S34300.raw

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153             115              120              125
154
155    Gly Ala Trp Thr Leu Arg Ala Cys His Leu Cys Arg Cys Ile Phe Gly
156        130              135              140
157
158    Ala Leu His Cys Leu Pro Leu Gln Thr Pro Asp Arg Cys Asp Pro Lys
159        145              150              155              160
160
161    Asp Phe Leu Ala Ser His Ala His Gly Pro Ser Ala Gly Gly Ala Pro
162                165              170              175
163
164    Ser Leu Leu Leu Leu Leu Pro Cys Ala Leu Leu His Arg Leu Leu Arg
165                180              185              190
166
167    Pro Asp Ala Pro Ala His Pro Arg Ser Leu Val Pro Ser Val Leu Gln
168        195              200              205
169
170    Arg Glu Arg Arg Pro Cys Gly Arg Pro Gly Leu Gly His Arg Leu
171        210              215              220
172
173
174    (2) INFORMATION FOR SEQ ID NO:3:
175
176        (i) SEQUENCE CHARACTERISTICS:
177            (A) LENGTH: 36 base pairs
178            (B) TYPE: nucleic acid
179            (C) STRANDEDNESS: single
180            (D) TOPOLOGY: linear
181
182       (ii) MOLECULE TYPE: DNA (genomic)
183
184
185
186
187       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
188
189    ACTCTTGGAT CCAATTTGGG AAACAGCTAT CAAAGA                      36
190
191    (2) INFORMATION FOR SEQ ID NO:4:
192
193        (i) SEQUENCE CHARACTERISTICS:
194            (A) LENGTH: 42 base pairs
195            (B) TYPE: nucleic acid
196            (C) STRANDEDNESS: single
197            (D) TOPOLOGY: linear
198
199       (ii) MOLECULE TYPE: DNA (genomic)
200
201
202
203
204       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
205
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INPUT SET: S34300.raw

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206   TACAACTCTA GACTATTATT TACAACATAG AAAATTAAAG GC                    42
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208   (2) INFORMATION FOR SEQ ID NO:5:
209
210       (i) SEQUENCE CHARACTERISTICS:
211           (A) LENGTH: 36 base pairs
212           (B) TYPE: nucleic acid
213           (C) STRANDEDNESS: single
214           (D) TOPOLOGY: linear
215
216       (ii) MOLECULE TYPE: DNA (genomic)
217
218
219
220
221       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
222
223   ACTCTTGGAT CCGCCATCAT GACCTGGAGG CACCAT                            36
224
225   (2) INFORMATION FOR SEQ ID NO:6:
226
227       (i) SEQUENCE CHARACTERISTICS:
228           (A) LENGTH: 42 base pairs
229           (B) TYPE: nucleic acid
230           (C) STRANDEDNESS: single
231           (D) TOPOLOGY: linear
232
233       (ii) MOLECULE TYPE: DNA (genomic)
234
235
236
237
238       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
239
240   TACAACTCTA GACTATTATT TACAACATAG AAAATTAAAG GC                    42
241
242   (2) INFORMATION FOR SEQ ID NO:7:
243
244       (i) SEQUENCE CHARACTERISTICS:
245           (A) LENGTH: 174 amino acids
246           (B) TYPE: amino acid
247           (C) STRANDEDNESS: single
248           (D) TOPOLOGY: linear
249
250       (ii) MOLECULE TYPE: protein
251
252
253
254
255       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
256
257       Met His Ala Ala Ile Ser Lys Val Phe Glu Leu Gly Leu Val Ala Gly
258       1               5                   10                  15
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/393,023A*

INPUT SET: S34300.raw

Line	Error	Original Text